

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/371,333DATE: 09/20/1999
TIME: 13:23:52

INPUT SET: S33395.raw

<p>This Raw Listing contains the General Information Section and up to the first 5 pages.</p>

SEQUENCE LISTING

1
2
3 (1) General Information
4
5 (i) APPLICANT: Xu, Wenfeng
6 Presnell, Scott R.
7 Yee, David P.
8 Foster, Donald C.
9
10 (ii) TITLE OF THE INVENTION: PROTEASE-ACTIVATED RECEPTOR
11 PAR4 (ZCHEMR2)
12
13 (iii) NUMBER OF SEQUENCES: 12
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: ZymoGenetics, Inc.
17 (B) STREET: 1201 Eastlake Avenue East
18 (C) CITY: Seattle
19 (D) STATE: WA
20 (E) COUNTRY: USA
21 (F) ZIP: 98102
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Diskette
25 (B) COMPUTER: IBM Compatible
26 (C) OPERATING SYSTEM: DOS
27 (D) SOFTWARE: FastSEQ for Windows Version 2.0
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: 09/371,333
31 (B) FILING DATE:
32 (C) CLASSIFICATION:
33
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: 09/053,866
36 (B) FILING DATE:
37
38
39 (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: Leith, Debra K
41 (B) REGISTRATION NUMBER: 32,619
42 (C) REFERENCE/DOCKET NUMBER: 98-10
43
44 (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: 206-442-6674
46 (B) TELEFAX: 206-442-6678

ENTERED

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47 (C) TELEX:

48

49

50 (2) INFORMATION FOR SEQ ID NO:1:

51

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 4895 base pairs

54 (B) TYPE: nucleic acid

55 (C) STRANDEDNESS: single

56 (D) TOPOLOGY: linear

57

58 (ix) FEATURE:

59

60 (A) NAME/KEY: Coding Sequence

61 (B) LOCATION: 176...1330

62 (D) OTHER INFORMATION:

63

64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

65

66 CTCCACGCGG CTGGCTGGCA AGCGGCCCTG GTGGGTCTGC GGGGGCAGGG GCAGCCTTCC 60

67 TGGTTTATCT CCACCGGCGC GATCTGCTCG TCCGCCTCGG CTCCAGAAGC TGGGGCTCAG 120

68 GGTCCGGCGA GGCAGGAAGC CTGAGGCCAC AGCCAGAGC AGCCTGAGTG CAGTC ATG 178

69 Met

70 1

71

72 TGG GGG CGA CTG CTC CTG TGG CCC CTG GTG CTG GGG TTC AGC CTG TCT 226

73 Trp Gly Arg Leu Leu Leu Trp Pro Leu Val Leu Gly Phe Ser Leu Ser

74 5 10 15

75

76 GGC GGC ACC CAG ACC CCC AGC GTC TAC GAC GAG AGC GGG AGC ACC GGA 274

77 Gly Gly Thr Gln Thr Pro Ser Val Tyr Asp Glu Ser Gly Ser Thr Gly

78 20 25 30

79

80 GGT GGT GAT GAC AGC ACG CCC TCA ATC CTG CCT GCC CCC CGC GGC TAC 322

81 Gly Gly Asp Asp Ser Thr Pro Ser Ile Leu Pro Ala Pro Arg Gly Tyr

82 35 40 45

83

84 CCA GGC CAA GTC TGT GCC AAT GAC AGT GAC ACC CTG GAG CTC CCG GAC 370

85 Pro Gly Gln Val Cys Ala Asn Asp Ser Asp Thr Leu Glu Leu Pro Asp

86 50 55 60 65

87

88 AGC TCA CGG GCA CTG CTT CTG GGC TGG GTG CCC ACC AGG CTG GTG CCC 418

89 Ser Ser Arg Ala Leu Leu Leu Gly Trp Val Pro Thr Arg Leu Val Pro

90 70 75 80

91

92 GCC CTC TAT GGG CTG GTC CTG GTG GTG GGG CTG CCG GCC AAT GGG CTG 466

93 Ala Leu Tyr Gly Leu Val Leu Val Val Gly Leu Pro Ala Asn Gly Leu

94 85 90 95

95

96 GCG CTG TGG GTG CTG GCC ACG CAG GCA CCT CGG CTG CCC TCC ACC ATG 514

97 Ala Leu Trp Val Leu Ala Thr Gln Ala Pro Arg Leu Pro Ser Thr Met

98 100 105 110

99

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100	CTG CTG ATG AAC CTC GCG ACT GCT GAC CTC CTG CTG GCC CTG GCG CTG	562
101	Leu Leu Met Asn Leu Ala Thr Ala Asp Leu Leu Leu Ala Leu Ala Leu	
102	115 120 125	
103		
104	CCC CCG CGG ATC GCC TAC CAC CTG CGT GGC CAG CGC TGG CCC TTC GGG	610
105	Pro Pro Arg Ile Ala Tyr His Leu Arg Gly Gln Arg Trp Pro Phe Gly	
106	130 135 140 145	
107		
108	GAG GCC GCC TGC CGC CTG GCC ACG GCC GCA CTC TAT GGT CAC ATG TAT	658
109	Glu Ala Ala Cys Arg Leu Ala Thr Ala Ala Leu Tyr Gly His Met Tyr	
110	150 155 160	
111		
112	GGC TCA GTG CTG CTG CTG GCC GCC GTC AGC CTG GAT CGC TAC CTG GCC	706
113	Gly Ser Val Leu Leu Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu Ala	
114	165 170 175	
115		
116	CTG GTG CAC CCG CTG CGG GCC CGC GCC CTG CGT GGC CGG CGC CTG GCC	754
117	Leu Val His Pro Leu Arg Ala Arg Ala Leu Arg Gly Arg Arg Leu Ala	
118	180 185 190	
119		
120	CTT GGA CTC TGC ATG GCT GCT TGG CTC ATG GCG GCC GCC CTG GCA CTG	802
121	Leu Gly Leu Cys Met Ala Ala Trp Leu Met Ala Ala Ala Leu Ala Leu	
122	195 200 205	
123		
124	CCC CTG ACA CTG CAG CGG CAG ACC TTC CGG CTG GCG CGC TCC GAT CGC	850
125	Pro Leu Thr Leu Gln Arg Gln Thr Phe Arg Leu Ala Arg Ser Asp Arg	
126	210 215 220 225	
127		
128	GTG CTC TGC CAT GAC GCG CTG CCC CTG GAC GCA CAG GCC TCC CAC TGG	898
129	Val Leu Cys His Asp Ala Leu Pro Leu Asp Ala Gln Ala Ser His Trp	
130	230 235 240	
131		
132		
133	CAA CCG GCC TTC ACC TGC CTG GCG CTG TTG GGC TGT TTC CTG CCC CTG	946
134	Gln Pro Ala Phe Thr Cys Leu Ala Leu Leu Gly Cys Phe Leu Pro Leu	
135	245 250 255	
136		
137	CTG GCC ATG CTG CTG TGC TAC GGG GCC ACC CTG CAC ACG CTG GCG GCC	994
138	Leu Ala Met Leu Leu Cys Tyr Gly Ala Thr Leu His Thr Leu Ala Ala	
139	260 265 270	
140		
141	AGC GGC CGG CGC TAC GGC CAC GCG CTG AGG CTG ACC GCA GTG GTG CTG	1042
142	Ser Gly Arg Arg Tyr Gly His Ala Leu Arg Leu Thr Ala Val Val Leu	
143	275 280 285	
144		
145	GCC TCC GCC GTG GCC TTC TTC GTG CCC AGC AAC CTG CTG CTG CTG CTG	1090
146	Ala Ser Ala Val Ala Phe Phe Val Pro Ser Asn Leu Leu Leu Leu Leu	
147	290 295 300 305	
148		
149	CAT TAC TCG GAC CCG AGC CCC AGC GCC TGG GGC AAC CTC TAT GGT GCC	1138
150	His Tyr Ser Asp Pro Ser Pro Ser Ala Trp Gly Asn Leu Tyr Gly Ala	
151	310 315 320	
152		

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153	TAC GTG CCC AGC CTG GCG CTG AGC ACC CTC AAC AGC TGC GTG GAT CCC	1186
154	Tyr Val Pro Ser Leu Ala Leu Ser Thr Leu Asn Ser Cys Val Asp Pro	
155	325 330 335	
156		
157	TTC ATC TAC TAC TAC GTG TCG GCC GAG TTC AGG GAC AAG GTG CGG GCA	1234
158	Phe Ile Tyr Tyr Tyr Val Ser Ala Glu Phe Arg Asp Lys Val Arg Ala	
159	340 345 350	
160		
161	GGG CTC TTC CAA CGG TCG CCG GGG GAC ACC GTG GCC TCC AAG GCC TCT	1282
162	Gly Leu Phe Gln Arg Ser Pro Gly Asp Thr Val Ala Ser Lys Ala Ser	
163	355 360 365	
164		
165	GCG GAA GGG GGC AGC CGG GGC ATG GGC ACC CAC TCC TCT TTG CTC CAG T	1331
166	Ala Glu Gly Gly Ser Arg Gly Met Gly Thr His Ser Ser Leu Leu Gln	
167	370 375 380 385	
168		
169	GACACAAAGT GGGGAAGGCT GTACTGGGTC GAACAGGGTC CCTTCCCCCA CTTACAGTCC	1391
170	TTCCTGGGAC CTCAGAATGT GACCTTATTT GGAAATAGGG TTGTTACAAC TGTCAGTAGC	1451
171	GGAGGTCAGT TTGGAGAAGG GTGGGCCCTTA CATCCAGTGT GGGTGGTGTG CTCATAAGAT	1511
172	AAGGAGAGGC CAGGCCTGGT GGCTCACGCC TGTAAATCCCA GCACTTTAAAG AGGCCAAGGC	1571
173	GGATGGATCA CTTGAGCCCA GGAGTTCAAC ACCAGCCTGA GCAACATGGT AAAACCCCAT	1631
174	CTCTACCAAA AATACAAAAA TTAGCTGGGC TTGGTGGCTG GCGCCTGTAA TCCCAGCTAC	1691
175	TCAGGAGACT GAGGCAGAAG GATCGCTTGA ACCTGGGAGG CAGAGGTTGC AGTGAGCCGA	1751
176	GATTGCGCCA CTGGACTCCA GCCTGCGTGA CAGAGAGCCT GTCTCTAAAT TAATTAATTA	1811
177	ATTAATTTAA TTCAATTTTA AAAAGACGAA AAGTGACGGC CAGGTGCAGT GGCTCACGCC	1871
178	TATAATCTCA GCACTCTGGG AGGCCAAGAT GGAGGATTGC TTGAAGCCAG GAGTTTGGGA	1931
179	CCAGCCTGGG CAACATAGGG GGATCCCATC TCTACACACA AAAAAATTTT TTAATGAACC	1991
180	AGGCATTGTG GCATGCGCCT ATAGTCCCAG CCACTCAAGA GGCACAGGCG GGAGGATCAC	2051
181	TTGAGCCTGG GAGGTTGTGG TTGCAGTGAG CTATGATTGT ACCACTGCAC TCCAGCCTGG	2111
182	GCAACAGAGC AAGACCTTGT CTCAAAAATA AACAACTAA AATTAAAAAA AGAAGACGAG	2171
183	AGATAGTGGG TGTGGTGGCT CACACCTGCA ATCCCAGCAC TTTGGAAGGC CGAGGTGGGC	2231
184	AGATCATCTG AGGCCAGGAG TTCAAGACCA GCCTGGCTAA CATGGTGAAG TCCTATCTCT	2291
185	ACCAAAAAATA CAAAAATTAG CCAGGCGTGG TGGTGGGCAC CTGTACTGGG GAGGTGCCCA	2351
186	CCCAGCTACT GGGGAGGCTG AGTCGCTTGA ATCGCTTGAA CCTGGGAGGC GAGGTTGCG	2411
187	GTCAGCTGAG ATGGTGCCAC TGCACTCCAG CCTGGGCGAA AGAGCGACTC TGTCTCCAAA	2471
188	AAAAAGAGAA GAGGAGAGGA CACAGAGACA CACAGAGAAG AAAGCCATGT GGCGGCAGAG	2531
189	GCAGAGATGG GAGTGATGCG GACGGACACA AACTAAGGGA TGCCACGATG CCAAGCACAG	2591
190	CCAACAGCCA CCAGCAGCCA GGAGACAGGC CTGGGACGGG CTCTCCCTCA CAGCCTCCAG	2651
191	AGGGAACAG CCCTGCCACC ACCTTGACCC TGGACTTCTG GCCTGCAGAA CTGTGAGACA	2711
192	ATAAACTCTC ATTGTTTTAA GCTGCCTGGC ATGTGGCACT TTGTCAGGGC AGCCCAGGAA	2771
193	TCTGAAACAG GATCAAATC TGCTTCCTGG GCCCTGCCAG CATCTCTGGC TCGGCTTTCT	2831
194	GGGCTGGATG CAGCCCACGA CGCACTGGTG TCTGAGATGG GGCTGGAGCT GGGGCTGGGG	2891
195	CTGCATTCCC TGGAGACTCA CTGCAAGTTC CTGCCCAGGA GGCTGAGGGC ACCCATCCT	2951
196	CAGTGCCCAA TGCTGTGGCC CCACCAGGCC CAGAGCCTGG TTGGCCATTC TCATGCCCAC	3011
197	CAGCTTCTGG CTTTGGGATG TCTCTTGAGC AACCAAGAATA GCACCCCCAA CTCTGCTCCC	3071
198	CAAAACCCAT CACTAGCACG GCTCAGCCTC CTGCTATCCC CTGACTGCTG GGGACCCCTCG	3131
199	CCTTCCCTCC TCTCACCTGC AGGCTGATCC TTCTTTTCAC TTTCTGTCAA TGTCACCAGG	3191
200	GATAAGGTGG GACAATGGGG GGTGGGGGTG GACAGTGTGT GCTGGGGGGT TCGGGTGCTG	3251
201	CAGACCTGGA ACTCCCTTCT GCCAGGATGT TGGCAGCCGG TTGTAAGCCT TGCACGGGAC	3311
202	AGACCACACC CACCGCAACC TCATCCCCTC AGCACTAACC ACATCCACTC TCAACCCCGT	3371
203	CCCCTTCGCA CTGACCACAC CCACCCCGTT CGGCCCCGCC CCCCAGCTG AACACTCCCG	3431
204	CCCTCAACCC CGCACCTCC GCACTCACCT CCCCCTCGCC GCTCGACCCC GCCCTCACCA	3491
205	CACTGACCAC CCTCAACCCA TTGCGCCAG TCCCCACCAC AGTGACCACA CCCTCACTGG	3551

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206 CTCGGCCCTG CCCCCAGTAT ACTGACCATT CCCCAGCCAC TTCCCTTCCG CACTTACCAC 3611
207 TCCCCAGCC ACGCCCCTCC CCGCTGACCG CTCCTCCAGC CCCGCCTCCC CCGTACAGGC 3671
208 AGAGCGCCCC CCCACCTCTA TGCTGCGTTC TCCTGACTTT ACGTTGGCCC CTCCTCTGCC 3731
209 AAGCCCCCAG GGGAGCCCTC CCTGGCGTCC GAGGGTGGGA GTCGGGGTGT GGCAGGCCGC 3791
210 GGTGGGGGGC GGCAGTGGCT CCGCGCACTC ACCCGGGCCC CGGGCAGGGG CGCGCTCCAC 3851
211 TTCGTTGCAC GCGGGTCCGG CGCACAGTTC CCGGGCGAGT GGGCTGTGCG TGCTGACGTT 3911
212 GTAGAAGCGA GTGGCCTCGA AGGCTACGGG ACGAGGGTGG CGGGTGACCA AGTGCAGGCG 3971
213 CGACGGGTCA GGGACCGGGC CGGGCCGGGG GTGCGGGCGC GCGGGCCTAC CGGGTTCGTA 4031
214 GTAGTCGTAC ACGGAGACTG GCAGCGCCGA CGTCCTGCCC ACCACGCACT CCCGGAGAGC 4091
215 ACGGAACCGC ACGCACGTCA GGCACCGGCT GGGGATCTGT GGGGCAGCGG CGGGCGCAGG 4151
216 CTCGACCCGG GCCAGGAGGC CCGGGGCGCT GAGCTCAGGC CCAGAACTGG CTGATTTTCAG 4211
217 GGATACCCAG GACGCGTGAA ACACAGAAGA AACGTGATCC CATTTTCTTT TTTTCTTTTA 4271
218 CTTTTCTTTT TTTTTTTTTT TCCTGAGACA GAGTCTCGCG CTGTTGCCCA GGCTGGAGTG 4331
219 CAGTGGCGTG ATCTCGGCTC ACTGCAAGCT CGGCCTCCTG GGTTCAAATG ATTCTCCTGC 4391
220 CTCAGCCTCC CAAGTAGCTG GGATAACAGG CGCCCACCAC CGCACCTGCT TAATTTTTTG 4451
221 TATTTTTGAT CAAGACGGAG TTTCACCATG TTGGCCAGGC TGGTCTCCAA CTCCTGCCCT 4511
222 CAAGTGATCC GCCTCGGTCC CATTTTTTAT TCTTTGGGTC CTTCCATCCC ACTGGGAAAA 4571
223 CGTCTCAGGT GGCCTCTGAA ACACCACTCC TTTTTGTGTG TGTGCACGCA TGGCTGAGCA 4631
224 TGTGTGGGTG GGAGTCAGCA CATTACGAT ACTGTGCAAT CATCACCTCT GTCTAGTTAC 4691
225 AGGACGGTTT CTTTCTCCCC CAAAGAAACC CCATCGCCAT CAGCACTCAC TCCCCACTCC 4751
226 CCCAGCCCCT GGCAACCACA AATCTTTCCA ACTCTACGGA TTTGCCTGTT CTGGGCATTT 4811
227 CATGTCAATG GAATCATGTA CTCTGTGAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 4871
228 AAAAAAAAAA AAAAAAAAAA AAAA
229

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

243 Met Trp Gly Arg Leu Leu Leu Trp Pro Leu Val Leu Gly Phe Ser Leu
244 1 5 10 15
245 Ser Gly Gly Thr Gln Thr Pro Ser Val Tyr Asp Glu Ser Gly Ser Thr
246 20 25 30
247 Gly Gly Gly Asp Asp Ser Thr Pro Ser Ile Leu Pro Ala Pro Arg Gly
248 35 40 45
249 Tyr Pro Gly Gln Val Cys Ala Asn Asp Ser Asp Thr Leu Glu Leu Pro
250 50 55 60
251 Asp Ser Ser Arg Ala Leu Leu Leu Gly Trp Val Pro Thr Arg Leu Val
252 65 70 75 80
253 Pro Ala Leu Tyr Gly Leu Val Leu Val Val Gly Leu Pro Ala Asn Gly
254 85 90 95
255 Leu Ala Leu Trp Val Leu Ala Thr Gln Ala Pro Arg Leu Pro Ser Thr
256 100 105 110
257 Met Leu Leu Met Asn Leu Ala Thr Ala Asp Leu Leu Leu Ala Leu Ala
258 115 120 125

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/371,333

DATE: 09/20/1999
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Line

Error

Original Text

PAGE: 1

SEQUENCE MISSING ITEM REPORT
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< < THERE ARE NO ITEMS MISSING > >

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/09/371,333

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Line	Original Text	Corrected Text
3	(1) General Information	(1) GENERAL INFORMATION:
10	(ii) TITLE OF THE INVENTION: PROTEASE-ACTIVAT	(ii) TITLE OF INVENTION: PROTEASE-ACTIVATED R